

After reading Ch 6 and completing the chapter exercises using their data, build a neighbor-joining tree using your own data from the past few weeks. Make sure to carefully assess each of the choices, including whether your Jukes-Cantor distance is low enough, as well as each of the options in the actual tree-building window. Take a screen shot or otherwise record which option you chose.

**My Jukes-Cantor distance was 0.20 using: Substitution model -> Nucleotide, Substitutions to Include -> All, Rates Among Sites -> Uniform Rates, Pattern among Lineages -> Same, Gaps/Missing Data Treatment -> Pairwise Deletion, and Select Codon Position -> 1<sup>st</sup>, 2<sup>nd</sup>, and 3<sup>rd</sup>.**

**For my NJ tree building, I chose: Scope -> All Taxa Selected, Statistical Method -> Neighbor-joining, Test of Phylogeny -> None, Substitution Type -> Nucleotide, Model/Method -> Maximum Composite Likelihood, Substitutions to Include -> d: Transitions + Transversions, Rates among Sites -> Uniform Rates, Pattern among Lineages -> Same, Gaps/Missing Data Treatment -> Pairwise Deletion, Select Codon Positions -> 1<sup>st</sup>, 2<sup>nd</sup>, and 3<sup>rd</sup>**

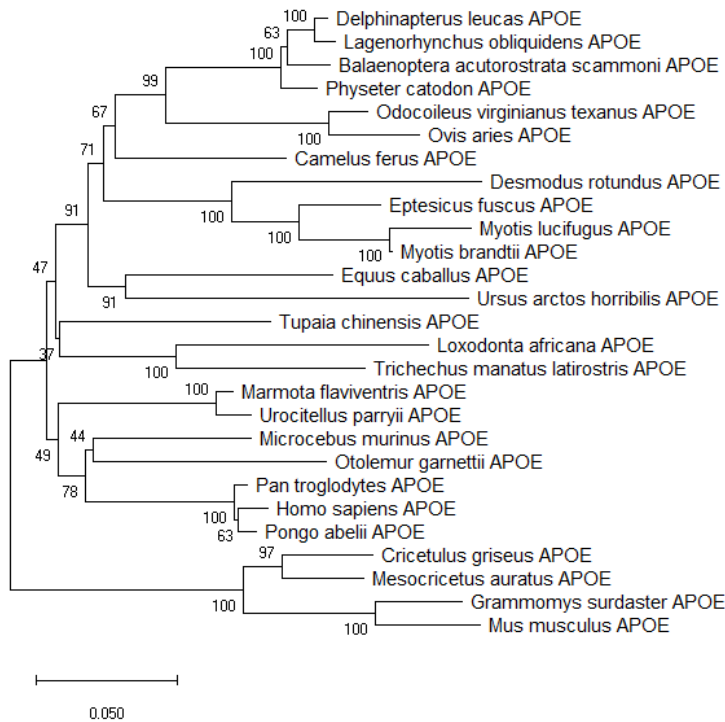
**Initial Tree:**



After you have constructed the tree, save a picture of the tree as your Initial Tree.

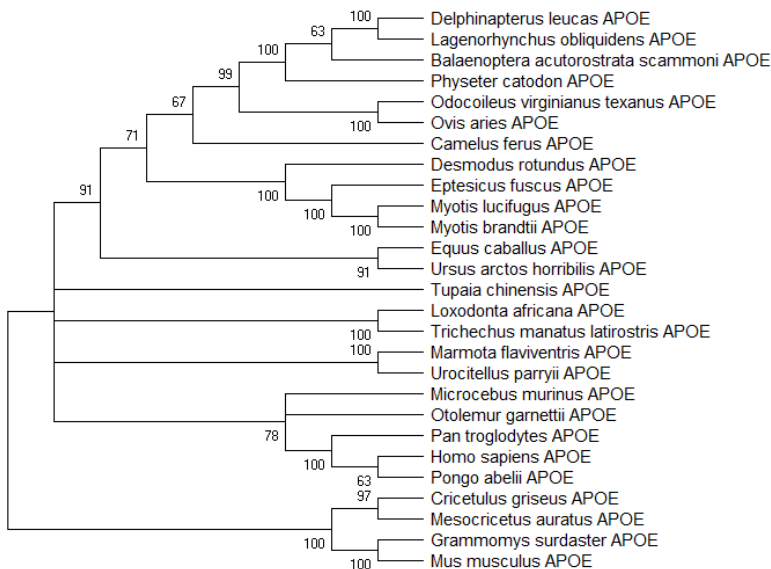
Then perform bootstrapping (at least 1000 replicates, unless your data set is so large that this really slows you down), and take a picture of the tree as Bootstrap Consensus.

## Bootstrap Consensus:



If some of the nodes have less than 50% support, collapse the nodes to create majority rule tree. Take a picture of the Majority Rule tree.

## Majority Rule Tree



Open a document and import all your trees into it. Discuss the options you chose to make the Initial Tree, then discuss whether bootstrapping lowered your confidence in the reproducibility of any of the nodes, and what this might mean for your project.

**Bootstrapping only lowered my confidence in the reproducibility of my “early” (left) nodes when organized in a rooted tree. However, as discussed in the textbook, the NJ method produces a non-rooted tree, thus it makes sense that the left most nodes are the ones with the least producibility, as there is no evolutionary root to base them off. I don’t think this means very much for my project, other than I am pretty confident in most of my external nodes.**

Overall, discuss what your final tree (Consensus or Majority Rule) tells you about your project and the data you are analyzing (in other words, you're constructing this tree for a purpose, to figure something out... what is the tree actually telling you?).

**My Majority Rule tree tells me that there are groupings of the APOE gene that have diverged from others and have formed clades of their own. Specifically, my tree shows me that with some measure of confidence, that the Homo sapiens APOE is (predicted) most evolutionarily similar to that of Pongo abelii, Pan troglodytes, Oryzomys latipes and Microcebus murinus. These give me a range of species to investigate further to determine if any of these species would be a good fit for a new model of Alzheimer’s disease.**

Upload that document here as your assignment for this week. Due Wednesday night (6/26) at midnight.